

## SEQUENCE LISTING

<110> Hellström, Mats  
Wallgard, Elisabet  
Kalén, Mattias

<120> ANGIOGENESIS-AFFECTING POLYPEPTIDES, PROTEINS, AND  
COMPOSITIONS, AND METHODS OF USE THEREOF

<130> 78063

<160> 52

<170> PatentIn version 3.2

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<212> DNA

<213> Murinae gen. sp.

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Arg Arg Thr Tyr Pro Arg Pro His Glu Tyr Leu Ser Pro Ala Asp Leu  
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Pro Lys Asn Trp Asp Trp Arg Asn Val Asn Gly Val Asn Tyr Ala Ser  
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Val Thr Arg Asn Gln His Ile Pro Gln Tyr Cys Gly Ser Cys Trp Ala  
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His Gly Ser Thr Ser Ala Met Ala Asp Arg Ile Asn Ile Lys Arg Lys  
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Glu Phe Lys Glu Cys His Thr Ile Gln Asn Tyr Thr Leu Trp Arg Val  
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Gly Asp Tyr Gly Ser Leu Ser Gly Arg Glu Lys Met Met Ala Glu Ile  
 195 200 205

Tyr Ala Asn Gly Pro Ile Ser Cys Gly Ile Met Ala Thr Glu Met Met  
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Ser Asn Tyr Thr Gly Gly Ile Tyr Ala Glu His Gln Asp Gln Ala Val  
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Lys Gly Trp Met Arg Ile Val Thr Ser Thr Tyr Lys Gly Gly Thr Gly  
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 <213> Homo sapiens

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Thr Tyr Pro Arg Pro His Glu Tyr Leu Ser Pro Ala Asp Leu Pro Lys  
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Arg Asn Gln His Ile Pro Gln Tyr Cys Gly Ser Cys Trp Ala His Ala  
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Ser Thr Ser Ala Met Ala Asp Arg Ile Asn Ile Lys Arg Lys Gly Ala  
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Trp Pro Ser Thr Leu Leu Ser Val Gln Asn Val Ile Asp Cys Gly Asn  
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Ala Gly Ser Cys Glu Gly Gly Asn Asp Leu Ser Val Trp Asp Tyr Ala  
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His Gln His Gly Ile Pro Asp Glu Thr Cys Asn Asn Tyr Gln Ala Lys  
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Asp Gln Glu Cys Asp Lys Phe Asn Gln Cys Gly Thr Cys Asn Glu Phe  
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Lys Glu Cys His Ala Ile Arg Asn Tyr Thr Leu Trp Arg Val Gly Asp  
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Tyr Gly Ser Leu Ser Gly Arg Glu Lys Met Met Ala Glu Ile Tyr Ala  
 195 200 205

Asn Gly Pro Ile Ser Cys Gly Ile Met Ala Thr Glu Arg Leu Ala Asn  
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Tyr Thr Gly Gly Ile Tyr Ala Glu Tyr Gln Asp Thr Thr Tyr Ile Asn  
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His Val Val Ser Val Ala Gly Trp Gly Ile Ser Asp Gly Thr Glu Tyr  
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Trp Ile Val Arg Asn Ser Trp Gly Glu Pro Trp Gly Glu Arg Gly Trp  
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Thr Ala Gly Pro Ser Cys Ser Leu Leu Gln Glu Ala Phe Arg Arg Tyr		
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Tyr Asn Tyr Val Phe Gly Phe Tyr Lys Arg His His Gly Pro Ala Arg		
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Phe Arg Ala Glu Pro Gln Leu Gln Lys Leu Leu Val Ser Ile Thr Leu		
100	105	110
Glu Ser Glu Cys Glu Ser Phe Pro Ser Leu Ser Ser Asp Glu Thr Tyr		
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Ser Leu Leu Val Gln Glu Pro Val Ala Val Leu Lys Ala Asn Ser Val		
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Trp Gly Ala Leu Arg Gly Leu Glu Thr Phe Ser Gln Leu Val Tyr Gln		
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Asp Ser Phe Gly Thr Phe Thr Ile Asn Glu Ser Ser Ile Ala Asp Ser		
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Pro Arg Phe Pro His Arg Gly Ile Leu Ile Asp Thr Ser Arg His Phe		
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Lys Phe Asn Val Leu His Trp His Ile Val Asp Asp Gln Ser Phe Pro		
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Tyr Gln Ser Thr Thr Phe Pro Glu Leu Ser Asn Lys Gly Ser Tyr Ser		
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Leu Ser His Val Tyr Thr Pro Asn Asp Val Arg Met Val Leu Glu Tyr		
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Ala Arg Leu Arg Gly Ile Arg Val Ile Pro Glu Phe Asp Thr Pro Gly		
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Tyr Asn Gln Lys Thr Lys Thr Gln Val Phe Gly Pro Val Asp Pro Thr  
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Val Asn Thr Thr Tyr Ala Phe Phe Asn Thr Phe Phe Lys Glu Ile Ser  
 305 310 315 320

Ser Val Phe Pro Asp Gln Phe Ile His Leu Gly Gly Asp Glu Val Glu  
 325 330 335

Phe Gln Cys Trp Ala Ser Asn Pro Asn Ile Gln Gly Phe Met Lys Arg  
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Lys Gly Phe Gly Ser Asp Phe Arg Arg Leu Glu Ser Phe Tyr Ile Lys  
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Lys Ile Leu Glu Ile Ile Ser Ser Leu Lys Lys Asn Ser Ile Val Trp  
 370 375 380

Gln Glu Val Phe Asp Asp Lys Val Glu Leu Gln Pro Gly Thr Val Val  
 385 390 395 400

Glu Val Trp Lys Ser Glu His Tyr Ser Tyr Glu Leu Lys Gln Val Thr  
 405 410 415

Gly Ser Gly Phe Pro Ala Ile Leu Ser Ala Pro Trp Tyr Leu Asp Leu  
 420 425 430

Ile Ser Tyr Gly Gln Asp Trp Lys Asn Tyr Tyr Lys Val Glu Pro Leu  
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Asn Phe Glu Gly Ser Glu Lys Gln Lys Gln Leu Val Ile Gly Gly Glu  
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Ala Cys Leu Trp Gly Glu Phe Val Asp Ala Thr Asn Leu Thr Pro Arg  
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Leu Trp Pro Arg Ala Ser Ala Val Gly Glu Arg Leu Trp Ser Pro Lys  
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Thr Val Thr Asp Leu Glu Asn Ala Tyr Lys Arg Leu Ala Val His Arg  
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<212> PRT

<213> Homo sapiens

<400> 10

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			20					25					30		

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 Ser Ala Lys Pro Gly Pro Ala Leu Trp Pro Leu Pro Leu Leu Val Lys  
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 Met Thr Pro Asn Leu Leu His Leu Ala Pro Glu Asn Phe Tyr Ile Ser  
 65 70 75 80  
 His Ser Pro Asn Ser Thr Ala Gly Pro Ser Cys Thr Leu Leu Glu Glu  
 85 90 95  
 Ala Phe Arg Arg Tyr His Gly Tyr Ile Phe Gly Phe Tyr Lys Trp His  
 100 105 110  
 His Glu Pro Ala Glu Phe Gln Ala Lys Thr Gln Val Gln Gln Leu Leu  
 115 120 125  
 Val Ser Ile Thr Leu Gln Ser Glu Cys Asp Ala Phe Pro Asn Ile Ser  
 130 135 140  
 Ser Asp Glu Ser Tyr Thr Leu Leu Val Lys Glu Pro Val Ala Val Leu  
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 Lys Ala Asn Arg Val Trp Gly Ala Leu Arg Gly Leu Glu Thr Phe Ser  
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 180 185 190  
 Thr Ile Ile Asp Ser Pro Arg Phe Ser His Arg Gly Ile Leu Ile Asp  
 195 200 205  
 Thr Ser Arg His Tyr Leu Pro Val Lys Ile Ile Leu Lys Thr Leu Asp  
 210 215 220  
 Ala Met Ala Phe Asn Lys Phe Asn Val Leu His Trp His Ile Val Asp  
 225 230 235 240  
 Asp Gln Ser Phe Pro Tyr Gln Ser Ile Thr Phe Pro Glu Leu Ser Asn  
 245 250 255  
 Lys Gly Ser Tyr Ser Leu Ser His Val Tyr Thr Pro Asn Asp Val Arg  
 260 265 270  
 Met Val Ile Glu Tyr Ala Arg Leu Arg Gly Ile Arg Val Leu Pro Glu

275		280		285
Phe Asp Thr Pro Gly His Thr Leu Ser Trp Gly Lys Gly Gln Lys Asp				
290		295		300
Leu Leu Thr Pro Cys Tyr Ser Arg Gln Asn Lys Leu Asp Ser Phe Gly				
305		310		320
Pro Ile Asn Pro Thr Leu Asn Thr Thr Tyr Ser Phe Leu Thr Thr Phe				
		325		330
Phe Lys Glu Ile Ser Glu Val Phe Pro Asp Gln Phe Ile His Leu Gly				
		340		345
Gly Asp Glu Val Glu Phe Lys Cys Trp Glu Ser Asn Pro Lys Ile Gln				
		355		360
Asp Phe Met Arg Gln Lys Gly Phe Gly Thr Asp Phe Lys Lys Leu Glu				
		370		375
Ser Phe Tyr Ile Gln Lys Val Leu Asp Ile Ile Ala Thr Ile Asn Lys				
		385		390
Gly Ser Ile Val Trp Gln Glu Val Phe Asp Asp Lys Ala Lys Leu Ala				
		405		410
Pro Gly Thr Ile Val Glu Val Trp Lys Asp Ser Ala Tyr Pro Glu Glu				
		420		425
Leu Ser Arg Val Thr Ala Ser Gly Phe Pro Val Ile Leu Ser Ala Pro				
		435		440
Trp Tyr Leu Asp Leu Ile Ser Tyr Gly Gln Asp Trp Arg Lys Tyr Tyr				
		450		455
Lys Val Glu Pro Leu Asp Phe Gly Gly Thr Gln Lys Gln Lys Gln Leu				
		465		470
Phe Ile Gly Gly Glu Ala Cys Leu Trp Gly Glu Tyr Val Asp Ala Thr				
		485		490
Asn Leu Thr Pro Arg Leu Trp Pro Arg Ala Ser Ala Val Gly Glu Arg				
		500		505
Leu Trp Ser Ser Lys Asp Val Arg Asp Met Asp Asp Ala Tyr Asp Arg				
		515		520

Leu Thr Arg His Arg Cys Arg Met Val Glu Arg Gly Ile Ala Ala Gln  
 530 535 540

Pro Leu Tyr Ala Gly Tyr Cys Asn His Glu Asn Met  
 545 550 555

<210> 11  
 <211> 676  
 <212> DNA  
 <213> Murinae gen. sp.

<220>  
 <221> misc\_feature  
 <222> (604)..(604)  
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ctccatcatc gggcgctgc tggaagtgc gggctcacgg cctgggaaga acgtgcagct  
 120

gacagagaac gagatccgtg gtctgtgcct caaatcccgg gagattttcc tgagccagcc  
 180

cattcttctg gagcttgagg cgccctcaa gatctgtggt gacatccatg gccagtacta  
 240

tgaccttcta cggctgtttg agtatggtgg cttccctcca gagagcaact acctcttctt  
 300

gggggattat gtagatcggg gcaagcagtc tttggagacc atctgcctgt tgctggccta  
 360

taagatcaga taccggaga atttctttct acttcgtggg aaccatgagt gtgccagcat  
 420

caaccgcatt tatggcttct atgatgaatg caagagaaga tacaacatca aactgtggaa  
 480

gacgttcaact gactgcttca actgcctgoc cattgcagcc attgtggatg agaagatctt  
 540

ctgctgccac gggggcctgt ctccagactt gcaatccatg gagcagatta ggcgtattat  
 600

gcnngccaca gacgtgcctg accagggcct actgtgtgat ctctgtggt ctgaccctga  
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caagaaatag cctcca  
 676

<210> 12  
 <211> 1369



&lt;212&gt; DNA

&lt;213&gt; Murinae gen. sp.

&lt;400&gt; 12

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cgagaagctc aacctggact ccatcatcgg gcgcctgctg gaagtgcagg gctcacggcc  
120

tgggaagaac gtgcagctga cagagaacga gatccgtggt ctgtgcctca aatcccggga  
180

gattttcctg agccagccca ttctttctgga gcttgaggcg ccctcaaga tctgtggtga  
240

catccatggc cagtactatg accttctacg gctgtttgag tatggtggct tccctccaga  
300

gagcaactac ctcttcttgg gggattatgt agatcggggc aagcagtctt tggagaccat  
360

ctgcctgttg ctggcctata agatcagata ccgggagaat ttctttctac ttogtgggaa  
420

ccatgagtgt gccagcatca accgcattta tggcttctat gatgaatgca agagaagata  
480

caacatcaaa ctgtggaaga cgttcaactga ctgcttcaac tgcctgcccc ttgcagccat  
540

tgtggatgag aagatcttct gctgccacgg gggcctgtct ccagacttgc aatccatgga  
600

gcagattagg cgtattatgc ggcccacaga cgtgcctgac cagggcctac tgtgtgatct  
660

cctgtggtct gaccctgaca aggatgttca aggctggggc gagaatgacc gtggtgtctc  
720

ctttaccttt ggggctgagg tggtagccaa gttcctgcac aagcatgatt tggacctcat  
780

ctgcagagca catcagggtg tagaagatgg ctatgagttc tttgccaaga gacagttggt  
840

gacactcttc tcagctccca actactgtgg agagtttgac aatgctggtg ccatgatgag  
900

tgtggatgag accctcatgt gttccttcca gatcctcaag ccgctgata agaataaggg  
960

caagtatggg cagttcagcg gcctgaaccc cggaggccgg cccatcactc caccocgcaa  
1020

ttctgccaaa gccaaagaaat agcctccatg tgctgccott ctgccccaga tcgtttgtac  
1080

agaaatcatg ctgccatggg tcacactggc ctctcaggcc caccgctcac ggggaacaca  
1140

cagcgttaag tgtctttcct ttatttttta aagaatcaat agcagcatct aatctcccag  
1200

ggctccctcc caccagcacc tgtggtggct gcaagtggaa tcctggggcc aaggctgcag  
1260

ctcagggcaa tggcagacca gattgtgggt ctccagcctt gcatggctgg cagccagatc  
1320

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1369

<210> 13  
<211> 330  
<212> PRT  
<213> Murinae gen. sp.

<400> 13

Met Ser Asp Ser Glu Lys Leu Asn Leu Asp Ser Ile Ile Gly Arg Leu  
1 5 10 15

Leu Glu Val Gln Gly Ser Arg Pro Gly Lys Asn Val Gln Leu Thr Glu  
20 25 30

Asn Glu Ile Arg Gly Leu Cys Leu Lys Ser Arg Glu Ile Phe Leu Ser  
35 40 45

Gln Pro Ile Leu Leu Glu Leu Glu Ala Pro Leu Lys Ile Cys Gly Asp  
50 55 60

Ile His Gly Gln Tyr Tyr Asp Leu Leu Arg Leu Phe Glu Tyr Gly Gly  
65 70 75 80

Phe Pro Pro Glu Ser Asn Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg  
85 90 95

Gly Lys Gln Ser Leu Glu Thr Ile Cys Leu Leu Leu Ala Tyr Lys Ile  
100 105 110

Arg Tyr Pro Glu Asn Phe Phe Leu Leu Arg Gly Asn His Glu Cys Ala  
115 120 125

Ser Ile Asn Arg Ile Tyr Gly Phe Tyr Asp Glu Cys Lys Arg Arg Tyr  
130 135 140

Asn Ile Lys Leu Trp Lys Thr Phe Thr Asp Cys Phe Asn Cys Leu Pro  
145 150 155 160

Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His Gly Gly Leu

165 170 175  
 Ser Pro Asp Leu Gln Ser Met Glu Gln Ile Arg Arg Ile Met Arg Pro  
 180 185 190  
 Thr Asp Val Pro Asp Gln Gly Leu Leu Cys Asp Leu Leu Trp Ser Asp  
 195 200 205  
 Pro Asp Lys Asp Val Gln Gly Trp Gly Glu Asn Asp Arg Gly Val Ser  
 210 215 220  
 Phe Thr Phe Gly Ala Glu Val Val Ala Lys Phe Leu His Lys His Asp  
 225 230 235 240  
 Leu Asp Leu Ile Cys Arg Ala His Gln Val Val Glu Asp Gly Tyr Glu  
 245 250 255  
 Phe Phe Ala Lys Arg Gln Leu Val Thr Leu Phe Ser Ala Pro Asn Tyr  
 260 265 270  
 Cys Gly Glu Phe Asp Asn Ala Gly Ala Met Met Ser Val Asp Glu Thr  
 275 280 285  
 Leu Met Cys Ser Phe Gln Ile Leu Lys Pro Ala Asp Lys Asn Lys Gly  
 290 295 300  
 Lys Tyr Gly Gln Phe Ser Gly Leu Asn Pro Gly Gly Arg Pro Ile Thr  
 305 310 315 320  
 Pro Pro Arg Asn Ser Ala Lys Ala Lys Lys  
 325 330

<210> 14  
 <211> 993  
 <212> DNA  
 <213> Homo sapiens

<400> 14  
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 120  
 aaatcccggg agatttttct gagccagccc attcttctgg agctggaggc acccctcaag  
 180  
 atctgcggtg acatacacgg ccagtactac gaccttctgc gactatttga gtatggcggt  
 240

ttccctcccg agagcaacta cctctttctg ggggactatg tggacagggg caagcagtcc  
300

ttggagacca tctgcctgct gctggcctat aagatcaagt acccgagaa cttcttcctg  
360

ctccgtggga accacgagtg tgccagcatc aaccgcatct atggtttcta cgatgagtgc  
420

aagagacgct acaacatcaa actgtggaaa acottcactg actgcttcaa ctgcctgccc  
480

atcgcgggcca tagtggacga aaagatcttc tgctgccacg gaggcctgtc cccggacctg  
540

cagtctatgg agcagattcg gcggatcatg cggccacag atgtgcctga ccagggcctg  
600

ctgtgtgacc tgctgtggtc tgaccctgac aaggacgtgc agggctgggg cgagaacgac  
660

cgtggcgtct cttttacctt tggagccgag gtggtggcca agttcctcca caagcacgac  
720

ttggacctca tctgccgagc acaccaggtg gtagaagacg gctacgagtt ctttgccaag  
780

cggcagctgg tgacactttt ctcagotccc aactactgtg gcgagtttga caatgctggc  
840

gccatgatga gtgtggacga gaccctcatg tgctctttcc agatcctcaa gcccgccgac  
900

aagaacaagg ggaagtacgg gcagttcagt ggcctgaacc ctggaggccg acccatcacc  
960

ccaccccgca attccgcca agccaagaaa tag  
993

<210> 15

<211> 330

<212> PRT

<213> Homo sapiens

<400> 15

Met	Ser	Asp	Ser	Glu	Lys	Leu	Asn	Leu	Asp	Ser	Ile	Ile	Gly	Arg	Leu
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Leu	Glu	Val	Gln	Gly	Ser	Arg	Pro	Gly	Lys	Asn	Val	Gln	Leu	Thr	Glu
			20					25					30		

Asn	Glu	Ile	Arg	Gly	Leu	Cys	Leu	Lys	Ser	Arg	Glu	Ile	Phe	Leu	Ser
		35					40					45			

Gln	Pro	Ile	Leu	Leu	Glu	Leu	Glu	Ala	Pro	Leu	Lys	Ile	Cys	Gly	Asp
	50					55					60				

Ile His Gly Gln Tyr Tyr Asp Leu Leu Arg Leu Phe Glu Tyr Gly Gly  
 65 70 75 80

Phe Pro Pro Glu Ser Asn Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg  
 85 90 95

Gly Lys Gln Ser Leu Glu Thr Ile Cys Leu Leu Leu Ala Tyr Lys Ile  
 100 105 110

Lys Tyr Pro Glu Asn Phe Phe Leu Leu Arg Gly Asn His Glu Cys Ala  
 115 120 125

Ser Ile Asn Arg Ile Tyr Gly Phe Tyr Asp Glu Cys Lys Arg Arg Tyr  
 130 135 140

Asn Ile Lys Leu Trp Lys Thr Phe Thr Asp Cys Phe Asn Cys Leu Pro  
 145 150 155 160

Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His Gly Gly Leu  
 165 170 175

Ser Pro Asp Leu Gln Ser Met Glu Gln Ile Arg Arg Ile Met Arg Pro  
 180 185 190

Thr Asp Val Pro Asp Gln Gly Leu Leu Cys Asp Leu Leu Trp Ser Asp  
 195 200 205

Pro Asp Lys Asp Val Gln Gly Trp Gly Glu Asn Asp Arg Gly Val Ser  
 210 215 220

Phe Thr Phe Gly Ala Glu Val Val Ala Lys Phe Leu His Lys His Asp  
 225 230 235 240

Leu Asp Leu Ile Cys Arg Ala His Gln Val Val Glu Asp Gly Tyr Glu  
 245 250 255

Phe Phe Ala Lys Arg Gln Leu Val Thr Leu Phe Ser Ala Pro Asn Tyr  
 260 265 270

Cys Gly Glu Phe Asp Asn Ala Gly Ala Met Met Ser Val Asp Glu Thr  
 275 280 285

Leu Met Cys Ser Phe Gln Ile Leu Lys Pro Ala Asp Lys Asn Lys Gly  
 290 295 300

Lys Tyr Gly Gln Phe Ser Gly Leu Asn Pro Gly Gly Arg Pro Ile Thr  
 305 310 315 320

Pro Pro Arg Asn Ser Ala Lys Ala Lys Lys  
 325 330

<210> 16  
 <211> 702  
 <212> DNA  
 <213> Murinae gen. sp.

<400> 16  
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 120

tctcagctat cacagcctta cagcaaagcc actatctctt tggattttga aattttctct  
 180

gccatgccta tgactatctt aaaattgggc aaagtatatc catttcagag gggctttttc  
 240

tgtactgaca acagcgtgaa gtaccogtac catgacagta ccatccogtc ccgtatactc  
 300

gccatactgg ggcttggctt acccattttc tctatgagta tggagaatct ctgtctgttt  
 360

actttaatgt cttgcattcg aattcctttg tcggcaatcc ctacatagcc accatttaca  
 420

aagccgtcgg agccttttgt tcggagtctc agctagtcag tccttgactg acatcgctaa  
 480

gtatactata ggcatgttgc ggccgcactt cttggctatc tgtaaccag actgggtcaaa  
 540

aatcaactgc agtgatggct atattgagga ctacatatgt caagggaatg aagagaaagt  
 600

caaggagggc aggttgtctt tctactcggg acactcttca ttctctatgt actgcatgct  
 660

gtttgtcgca ctttatcttc aagccaggat gaagggagac tg  
 702

<210> 17  
 <211> 1432  
 <212> DNA  
 <213> Murinae gen. sp.

<400> 17  
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120

gcagggcggc ccaatccaaa ctgccctggc ccctgctccc gtcagtctaa gaggctcgca  
180

gtcgcttggg gcggccgcca tcccaggggc ggggctctgg gaattgggta tctggaccgc  
240

cgcggtctgt tcctcccgcc actcgcacca ggtggtgaca ccatccagcc ggtgaccatg  
300

ttcgacaaga cgcggtctgc gtacgtggcc ctogatgtga tttgcgtggt gctggctgga  
360

ttgccttttg caattcttac ttcaaggcat acccccttcc agcgaggaat attctgtaat  
420

gatgactcca tcaagtaccc ttacaaggaa gacaccatac cttatgcctt attaggtgga  
480

atagtcattc cattctgtat tatcgttatg agtattggag aatctctgtc tgtttacttt  
540

aatgtcttgc attcgaattc ctttgtcggc aatccctaca tagccaccat ttacaaagcc  
600

gtcggagcct ttttgttcgg agtctcagct agtcagtcct tgactgacat cgctaagtat  
660

actataggca gtttgcggcc gcacttcttg gctatctgta acccagactg gtcaaaaatc  
720

aactgcagtg atggctatat tgaggactac atatgtcaag ggaatgaaga gaaagtcaag  
780

gagggcaggt tgtctttcta ctcgggacac tcttcattct ctatgtactg catgctgttt  
840

gtcgcacttt atcttcaagc caggatgaag ggagactggg caagactctt acgacccatg  
900

ctccagtttg ggctcattgc tttttccata tatgtgggcc tttctcgagt gtctgactac  
960

aaacaccaact ggagtgcgt cacagttgga ctcatcagg gagctgctat ggctatactg  
1020

gttgctttgt atgtatccga tttcttcaag gacacacatt cttacaaaga gagaaaggaa  
1080

gaggatccac acacgactct ccatgaaacc gccagttcac ggaactactg ggcgctggcc  
1140

cgcttcaaag gcaacagctg gaggctaaag gcagggggat gcgtattact tcctgctgta  
1200

cagaccattc tataaaggac tgctgctatc tatacctcct ggatgcccat tttatgtgtg  
1260

tacagttact tctaacacaa tgagtaacag ttcaattaaa gaaaatgaag cctgtcacta  
1320

aaacactgtc ccacctgtac atttttattg aaagacgcta tgtacaaatg tgtatgttac  
1380

atgccttctc agaatgatgt tgacttaaata ataataaaaa gcttgtgaac ca  
1432

<210> 18  
<211> 378  
<212> PRT  
<213> Murinae gen. sp.

<400> 18

Glu Ser Arg Arg Leu Arg Arg Gln Ile Gly Gly His Ser Val Ala Gly  
1 5 10 15

Arg Pro Asn Pro Asn Cys Pro Gly Pro Cys Ser Arg Gln Ser Lys Arg  
20 25 30

Leu Ala Val Ala Trp Gly Gly Arg His Pro Glu Gly Gly Ala Leu Gly  
35 40 45

Ile Gly Tyr Leu Asp Arg Arg Gly Leu Phe Leu Pro Pro Leu Ala Pro  
50 55 60

Gly Gly Asp Thr Ile Gln Pro Val Thr Met Phe Asp Lys Thr Arg Leu  
65 70 75 80

Pro Tyr Val Ala Leu Asp Val Ile Cys Val Leu Leu Ala Gly Leu Pro  
85 90 95

Phe Ala Ile Leu Thr Ser Arg His Thr Pro Phe Gln Arg Gly Ile Phe  
100 105 110

Cys Asn Asp Asp Ser Ile Lys Tyr Pro Tyr Lys Glu Asp Thr Ile Pro  
115 120 125

Tyr Ala Leu Leu Gly Gly Ile Val Ile Pro Phe Cys Ile Ile Val Met  
130 135 140

Ser Ile Gly Glu Ser Leu Ser Val Tyr Phe Asn Val Leu His Ser Asn  
145 150 155 160

Ser Phe Val Gly Asn Pro Tyr Ile Ala Thr Ile Tyr Lys Ala Val Gly  
165 170 175



Ala Phe Leu Phe Gly Val Ser Ala Ser Gln Ser Leu Thr Asp Ile Ala  
                   180                  185                  190

Lys Tyr Thr Ile Gly Ser Leu Arg Pro His Phe Leu Ala Ile Cys Asn  
                   195                  200                  205

Pro Asp Trp Ser Lys Ile Asn Cys Ser Asp Gly Tyr Ile Glu Asp Tyr  
                   210                  215                  220

Ile Cys Gln Gly Asn Glu Glu Lys Val Lys Glu Gly Arg Leu Ser Phe  
                   225                  230                  235                  240

Tyr Ser Gly His Ser Ser Phe Ser Met Tyr Cys Met Leu Phe Val Ala  
                   245                  250                  255

Leu Tyr Leu Gln Ala Arg Met Lys Gly Asp Trp Ala Arg Leu Leu Arg  
                   260                  265                  270

Pro Met Leu Gln Phe Gly Leu Ile Ala Phe Ser Ile Tyr Val Gly Leu  
                   275                  280                  285

Ser Arg Val Ser Asp Tyr Lys His His Trp Ser Asp Val Thr Val Gly  
                   290                  295                  300

Leu Ile Gln Gly Ala Ala Met Ala Ile Leu Val Ala Leu Tyr Val Ser  
                   305                  310                  315                  320

Asp Phe Phe Lys Asp Thr His Ser Tyr Lys Glu Arg Lys Glu Glu Asp  
                   325                  330                  335

Pro His Thr Thr Leu His Glu Thr Ala Ser Ser Arg Asn Tyr Trp Ala  
                   340                  345                  350

Leu Ala Arg Phe Lys Gly Asn Ser Trp Arg Leu Lys Ala Gly Gly Cys  
                   355                  360                  365

Val Leu Leu Pro Ala Val Gln Thr Ile Leu  
                   370                  375

<210> 19

<211> 1626

<212> DNA

<213> Homo sapiens

<400> 19

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120

caggccgtgc cggctgagga ggtcctgagg ctacagagct gccgcggctg gcacacgagc  
180

gcctcggcac taaccgagtg ttccgcgggg ctgtgagggg agggccccgg gcgccattgc  
240

tggcgggtggg agcgcgcgcc ggtctcagcc cgccctcggc tgctctctc ctccggctgg  
300

gaggggcccgt agctcggggc cgtcgcacgc cccggccccg gctcgagaat caagggcctc  
360

ggccgcgcgtc ccgcagctca gtccatcgcc cttgccgggc agcccgggca gagaccatgt  
420

ttgacaagac gcggctgccg tacgtggccc tcgatgtgct ctgcgtgttg ctggcttcca  
480

tgccatattgc tgttctaaaa ttggggccaaa tataatccatt tcagagaggc tttttctgta  
540

aagacaacag catcaactat ccgtaccatg acagtaccgt cacatccact gtcctcatcc  
600

tagtgggggt tggcttgccc atttcctcta ttattcttgg agaaaccctg tctgtttact  
660

gtaacctttt gcactcaaatt tcctttatca ggaataacta catagccact atttacaag  
720

ccattggaac ctttttattt ggtgcagctg ctagtcagtc cctgactgac attgccaagt  
780

attcaatagg cagactgcgg cctcacttct tggatgtttg tgatccagat tgggtcaaaaa  
840

tcaactgcag cgatggttac attgaatact acatatgtcg agggaatgca gaaagagtta  
900

aggaaggcag gttgtccttc tattcaggcc actcttcgtt ttccatgtac tgcattgtgt  
960

ttgtggcact ttatcttcaa gccaggatga agggagactg ggcaagactc ttacgcccc  
1020

cactgcaatt tgggtcttgt gccgtatcca tttatgtggg cttttctcga gtttctgatt  
1080

ataaacacca ctggagcgat gtgttgactg gaactattca gggagctctg gttgcaatat  
1140

tagttgctgt atatgtatcg gatttcttca aagaaagaac ttctttttaa gaaagaaaag  
1200

aggaggactc tcatacaact ctgcatgaaa caccaacaac tgggaatcac tatccgagca  
1260

atcaccagcc ttgaaaggca gcagggtgcc caggtgaagc tggcctgttt tctaaaggaa  
1320

aatgattgcc acaaggcaag aggatgcatc tttcttcctg gtgtacaagc ctttaaagac  
1380

ttctgctgct gctatgcctc ttggatgcac actttgtgtg tacatagtta cctttaactc  
1440

agtggttatc taatagctct aaactcatta aaaaaactcc aagccttcca ccaaaacagt  
1500

gccccacctg tatacatctt tattaaaaaa atgtaatgct tatgtataaa catgtatgta  
1560

atatgctttc tatgaatgat gtttgattta aatataatac atattaaaat gtatgggaga  
1620

accaaa  
1626

<210> 20  
<211> 378  
<212> PRT  
<213> Homo sapiens

<400> 20

Gly	Gly	Pro	Glu	Ala	Thr	Glu	Leu	Pro	Arg	Leu	Ala	His	Glu	Arg	Leu
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Gly	Thr	Asn	Arg	Val	Phe	Ala	Gly	Ala	Val	Arg	Gly	Gly	Pro	Arg	Ala
		20					25						30		

Pro	Leu	Leu	Ala	Val	Gly	Ala	Pro	Pro	Gly	Leu	Ser	Pro	Pro	Ser	Ala
		35					40					45			

Ala	Leu	Leu	Leu	Arg	Leu	Gly	Gly	Ala	Val	Ala	Arg	Gly	Arg	Arg	Gln
	50					55					60				

Pro	Arg	Pro	Gly	Leu	Glu	Asn	Gln	Gly	Pro	Arg	Pro	Pro	Ser	Arg	Ser
65					70					75					80

Ser	Val	His	Arg	Pro	Cys	Arg	Ala	Ala	Arg	Ala	Glu	Thr	Met	Phe	Asp
				85					90					95	

Lys	Thr	Arg	Leu	Pro	Tyr	Val	Ala	Leu	Asp	Val	Leu	Cys	Val	Leu	Leu
			100					105					110		

Ala	Ser	Met	Pro	Met	Ala	Val	Leu	Lys	Leu	Gly	Gln	Ile	Tyr	Pro	Phe
		115					120					125			

Gln Arg Gly Phe Phe Cys Lys Asp Asn Ser Ile Asn Tyr Pro Tyr His  
 130 135 140

Asp Ser Thr Val Thr Ser Thr Val Leu Ile Leu Val Gly Val Gly Leu  
 145 150 155 160

Pro Ile Ser Ser Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr Cys Asn  
 165 170 175

Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala Thr Ile  
 180 185 190

Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala Ser Gln Ser  
 195 200 205

Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro His Phe  
 210 215 220

Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser Asp Gly  
 225 230 235 240

Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val Lys Glu  
 245 250 255

Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met Tyr Cys  
 260 265 270

Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly Asp Trp  
 275 280 285

Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala Val Ser  
 290 295 300

Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His Trp Ser  
 305 310 315 320

Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile Leu Val  
 325 330 335

Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe Lys Glu  
 340 345 350

Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro Thr Thr  
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Gly Asn His Tyr Pro Ser Asn His Gln Pro

370

375

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 180  
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 720  
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 <212> PRT  
 <213> Homo sapiens

<400> 22

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Arg His Thr Pro Phe Gln Arg Gly Val Phe Cys Asn Asp Glu Ser Ile  
                   20                  25                  30

Lys Tyr Pro Tyr Lys Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly  
                   35                  40                  45

Ile Ile Ile Pro Phe Ser Ile Ile Val Ile Ile Leu Gly Glu Thr Leu  
           50                  55                  60

Ser Val Tyr Cys Asn Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn  
   65                  70                  75                  80

Tyr Ile Ala Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala  
                   85                  90                  95

Ala Ala Ser Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg  
                  100                 105                 110

Leu Arg Pro His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile  
           115                 120                 125

Asn Cys Ser Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala  
   130                 135                 140

Glu Arg Val Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser  
  145                 150                 155                 160

Phe Ser Met Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg  
           165                 170                 175

Met Lys Gly Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly  
           180                 185                 190

Leu Val Ala Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr  
           195                 200                 205

Lys His His Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu  
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Val Ala Ile Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg  
  225                 230                 235                 240

Thr Ser Phe Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His  
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Glu Thr Pro Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro  
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 660  
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 720  
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<211> 1052  
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<213> Murinae gen. sp.

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180  
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240  
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300  
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360  
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540  
cgctgcagca gtatgcactt cttggtagca gaatggaatg aaccatctat caacttctac  
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aaaagaagag gtgcttcgga tctgtccagt gaagagggat ggaggctctt caagattgac  
660  
aaagagtact tgctaaaaat ggcagcagag gagtgaggcg tgccggtgta gacaatgaca  
720  
acctccattg tgcttttagaa taattctcag cttcccttgc tttctatctt gtgtgtagtg  
780  
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840  
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900  
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960  
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<211> 171  
 <212> PRT  
 <213> Murinae gen. sp.

<400> 25

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Gln Val Ile Leu Thr Glu Lys Asp Leu Gln Glu Asp Gly Phe Gly Glu  
 35 40 45

His Pro Phe Tyr His Cys Leu Val Ala Glu Val Pro Lys Glu His Trp  
 50 55 60

Thr Pro Glu Gly His Ser Ile Val Gly Phe Ala Met Tyr Tyr Phe Thr  
 65 70 75 80

Tyr Asp Pro Trp Ile Gly Lys Leu Leu Tyr Leu Glu Asp Phe Phe Val  
 85 90 95

Met Ser Asp Tyr Arg Gly Phe Gly Ile Gly Ser Glu Ile Leu Lys Asn  
 100 105 110

Leu Ser Gln Val Ala Met Lys Cys Arg Cys Ser Ser Met His Phe Leu  
 115 120 125

Val Ala Glu Trp Asn Glu Pro Ser Ile Asn Phe Tyr Lys Arg Arg Gly  
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Ala Ser Asp Leu Ser Ser Glu Glu Gly Trp Arg Leu Phe Lys Ile Asp  
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Lys Glu Tyr Leu Leu Lys Met Ala Ala Glu Glu  
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<210> 26  
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 <212> DNA  
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<400> 26

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240

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tgctagaaga tggtttttga gagcaccctt tttaccactg cctggttgca gaagtgccga  
360

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420

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540

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660

ccagtgaaga gggttggaga ctgttcaaga tcgacaagga gtacttgcta aaaatggcaa  
720

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780

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840

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900

tcagatgcag tttggagagt cagatctttc tccttgaata tctttcgata aacaacaagg  
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1080

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<210> 27

<211> 190

<212> PRT

<213> Homo sapiens

<400> 27

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Thr	Ala	Ala 35	Asp	Cys	Ser	Asp	Ile 40	Leu	Arg	Leu	Ile	Lys 45	Glu	Leu	Ala
Lys	Tyr 50	Glu	Tyr	Met	Glu	Glu 55	Gln	Val	Ile	Leu	Thr 60	Glu	Lys	Asp	Leu
Leu 65	Glu	Asp	Gly	Phe	Gly 70	Glu	His	Pro	Phe	Tyr 75	His	Cys	Leu	Val	Ala 80
Glu	Val	Pro	Lys	Glu 85	His	Trp	Thr	Pro	Glu 90	Gly	Asn	Pro	Ser	Pro 95	Phe
Pro	Glu	Ala	Arg 100	Glu	Thr	Asn	Ile	Val 105	Gly	Phe	Ala	Met	Tyr 110	Tyr	Phe
Thr	Tyr	Asp 115	Pro	Trp	Ile	Gly	Lys 120	Leu	Leu	Tyr	Leu	Glu 125	Asp	Phe	Phe
Val	Met 130	Ser	Asp	Tyr	Arg	Gly 135	Thr	Ile	Glu	Leu	Trp 140	His	Arg	Ile	Arg
Asn 145	Ser	Glu	Glu	Ser	Lys 150	Pro	Gly	Cys	Asn	Glu 155	Val	Ser	Leu	Ala	Ala 160
Cys	Thr	Ser	Trp	Ala 165	Glu	Trp	Asn	Glu	Pro 170	Ser	Ile	Asn	Phe	Tyr 175	Lys
Arg	Arg	Gly	Ala 180	Ser	Asp	Leu	Ser	Ser 185	Glu	Glu	Gly	Trp	Arg 190		

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<211> 745
<212> DNA
<213> Murinae gen. sp.

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180
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240

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300

ggcgccatga tgagtgtgga tgagaccctc atgtgttcct tccagatttt aaagcctgca  
360

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caagcaaaga aatagatgtc acttgacact gcctgggttg gacttgtaac atagcgttca  
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cattctcaag agagcatttg gttctgaacc totgttcctt ttgtggacag ctctgatgat  
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<210> 29

<211> 2127

<212> DNA

<213> Murinae gen. sp.

<400> 29

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120

tccaggagaa cgagatccga ggactctgcc tgaagtctcg ggagatcttc ctcaagtcagc  
180

ctatcctttt agaacttgaa gcaccactca agatatgtgg tgacatccac gggcagtact  
240

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420

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600

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960

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1140

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1380

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1440

gtttgaaagg gactgcttcc cctcattgtc ttgtcatgta caaactagtg tctgcagctg  
1500

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1560

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1800

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2040

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<211> 323

<212> PRT

<213> Murinae gen. sp.

<400> 30

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Asn	Glu	Ile	Arg	Gly	Leu	Cys	Leu	Lys	Ser	Arg	Glu	Ile	Phe	Leu	Ser
		35					40					45			

Gln	Pro	Ile	Leu	Leu	Glu	Leu	Glu	Ala	Pro	Leu	Lys	Ile	Cys	Gly	Asp
	50					55					60				

Ile	His	Gly	Gln	Tyr	Tyr	Asp	Leu	Leu	Arg	Leu	Phe	Glu	Tyr	Gly	Gly
65					70					75					80

Phe	Pro	Pro	Glu	Ser	Asn	Tyr	Leu	Phe	Leu	Gly	Asp	Tyr	Val	Asp	Arg
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Gly	Lys	Gln	Ser	Leu	Glu	Thr	Ile	Cys	Leu	Leu	Leu	Ala	Tyr	Lys	Ile
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Lys	Tyr	Pro	Glu	Asn	Phe	Phe	Leu	Leu	Arg	Gly	Asn	His	Glu	Cys	Ala
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 Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His Gly Gly Leu  
                                     165                                      170                                      175  
 Ser Pro Asp Leu Gln Ser Met Glu Gln Ile Arg Arg Ile Met Arg Pro  
                                     180                                      185                                      190  
 Thr Asp Val Pro Asp Gln Gly Leu Leu Cys Asp Leu Leu Trp Ser Asp  
     195                                      200                                      205  
 Pro Asp Lys Asp Val Leu Gly Trp Gly Glu Asn Asp Arg Gly Val Ser  
     210                                      215                                      220  
 Phe Thr Phe Gly Ala Glu Val Val Ala Lys Phe Leu His Lys His Asp  
     225                                      230                                      235                                      240  
 Leu Asp Leu Ile Cys Arg Ala His Gln Val Val Glu Asp Gly Tyr Glu  
                                     245                                      250                                      255  
 Phe Phe Ala Lys Arg Gln Leu Val Thr Leu Phe Ser Ala Pro Asn Tyr  
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 Cys Gly Glu Phe Asp Asn Ala Gly Ala Met Met Ser Val Asp Glu Thr  
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 Leu Met Cys Ser Phe Gln Ile Leu Lys Pro Ala Glu Lys Lys Lys Pro  
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 Ala Lys Lys

<210> 31  
 <211> 993  
 <212> DNA  
 <213> Homo sapiens  
 <400> 31

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180

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240

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300

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420

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780

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<210> 32  
<211> 330  
<212> PRT  
<213> Homo sapiens

<400> 32

Met	Ser	Asp	Ser	Glu	Lys	Leu	Asn	Leu	Asp	Ser	Ile	Ile	Gly	Arg	Leu
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Leu Glu Val Gln Gly Ser Arg Pro Gly Lys Asn Val Gln Leu Thr Glu  
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 Asn Glu Ile Arg Gly Leu Cys Leu Lys Ser Arg Glu Ile Phe Leu Ser  
 35 40 45  
 Gln Pro Ile Leu Leu Glu Leu Glu Ala Pro Leu Lys Ile Cys Gly Asp  
 50 55 60  
 Ile His Gly Gln Tyr Tyr Asp Leu Leu Arg Leu Phe Glu Tyr Gly Gly  
 65 70 75 80  
 Phe Pro Pro Glu Ser Asn Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg  
 85 90 95  
 Gly Lys Gln Ser Leu Glu Thr Ile Cys Leu Leu Leu Ala Tyr Lys Ile  
 100 105 110  
 Lys Tyr Pro Glu Asn Phe Phe Leu Leu Arg Gly Asn His Glu Cys Ala  
 115 120 125  
 Ser Ile Asn Arg Ile Tyr Gly Phe Tyr Asp Glu Cys Lys Arg Arg Tyr  
 130 135 140  
 Asn Ile Lys Leu Trp Lys Thr Phe Thr Asp Cys Phe Asn Cys Leu Pro  
 145 150 155 160  
 Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His Gly Gly Leu  
 165 170 175  
 Ser Pro Asp Leu Gln Ser Met Glu Gln Ile Arg Arg Ile Met Arg Pro  
 180 185 190  
 Thr Asp Val Pro Asp Gln Gly Leu Leu Cys Asp Leu Leu Trp Ser Asp  
 195 200 205  
 Pro Asp Lys Asp Val Gln Gly Trp Gly Glu Asn Asp Arg Gly Val Ser  
 210 215 220  
 Phe Thr Phe Gly Ala Glu Val Val Ala Lys Phe Leu His Lys His Asp  
 225 230 235 240  
 Leu Asp Leu Ile Cys Arg Ala His Gln Val Val Glu Asp Gly Tyr Glu  
 245 250 255

Phe Phe Ala Lys Arg Gln Leu Val Thr Leu Phe Ser Ala Pro Asn Tyr  
260 265 270

Cys Gly Glu Phe Asp Asn Ala Gly Ala Met Met Ser Val Asp Glu Thr  
275 280 285

Leu Met Cys Ser Phe Gln Ile Leu Lys Pro Ala Asp Lys Asn Lys Gly  
290 295 300

Lys Tyr Gly Gln Phe Ser Gly Leu Asn Pro Gly Gly Arg Pro Ile Thr  
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Pro Pro Arg Asn Ser Ala Lys Ala Lys Lys  
325 330

<210> 33  
<211> 747  
<212> DNA  
<213> Murinae gen. sp.

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120

tgcgtatttg ttgagctggg agagtagccc agtggtacag cgcccacctg gaatacttga  
180

ggacctgggg ttgtctccca gcaactgcaaa aggaaaattc actgttacag tcttccttgc  
240

acttaaacca gctttgtcta ttgttttttt ggtttggctt tgttactttt gttgctgnnt  
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420

tcccaagtgc tgggaataat ggtgtggtca ccaccgcca gccttttgtc tatttttaaa  
480

cttgaaagaa acaacagccc agatttcaaa aataatataa tgcacttata cctaaaaaaa  
540

caaccaggag tgcccagtta ataacatddd ttaaatgtgg ggatgggaag ggcattagag  
600

gagtcttcct tctattgaag attcattaaa gtatttaaga tatgcccttt cactctttat  
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<210> 34

<211> 2021

<212> DNA

<213> Murinae gen. sp.

<400> 34

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120

agttccaagc tctctgggaa ccggaacggc agggaaagcc gagcgggcgg cctgaaggag  
180

agaagcaatg gatcagaggg ggctccaagt gaaggaaggg taagtccaaa gagcagcgtt  
240

cctgagactg gcctgataga ctgcagcact tcacaggccg ccagttctcc agaaccaacc  
300

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360

ggtgctggca gccattccga cgcttgaaga aaactgtctc gttccccccag aagcacatgt  
420

atgtttacact ggagatgacc aactgatttg tcttataaag gccactgttg agctgggaga  
480

gtagcccagt ggtacagcgc ccacctggaa tacttgagga cctgggggttg tctcccagca  
540

ctgcaaaagg aaaattcact gttacagtct tccttgact taaaccagct ttgtctattg  
600

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780

gaataatggg gtggtcacca ctgcccagcc ttttgtctgt ttttaaaactt gaaagaaaca  
840

acagcccaga ttccaataat aatataatgc atttatacct aaaaaaccaa ccaggagtgc  
900

ccagttaata acacttttta aatgtgggga tgggaagggc attagaggag tcttccttct  
960

attgaagatt cattaaagta tttaagata tgctctttca ctctttatat aaatccaaga  
1020

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1080

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1140

gatgttttct tactatttta gctactttgc gactgtgata gctgttacac tggattttta  
1200

aaaaacttgt acagcagcct ctttacagta aaaagagtgg gtgtcacact gaaaggctctg  
1260

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1320

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1380

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1440

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1500

aactcactgt gtgggtgctc ttggctgtct ggtgttcagt ctgtcccagg caggtcacag  
1560

agatctcccc ctctgcagcc cactcatctc tcccaagcca ccacactcag cttttatctg  
1620

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1680

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1740

aagggcagag tcagagttgg gcaggaagag tgtagtgcag cagatgcagc gtgaagacac  
1800

tgaagggtgt aagacagcgt ctcagtgtcg gtcctcctta aggattatct cgccagcgag  
1860

gttttcttag atactttgat cccattggag ctctgttaaa gtttaaaatg aaaattatca  
1920

tgtactgtat gggaaatgta aatactaact tttccacata tgtaaacttc agacacaaat  
1980

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2021

<210> 35  
 <211> 709  
 <212> PRT  
 <213> Murinae gen. sp.

<400> 35

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 20 25 30

Met Lys Met Thr Tyr Asn Met Thr Phe Phe Pro Asn Leu Met Gly His  
 35 40 45

Tyr Asp Gln Gly Ile Ala Ala Val Glu Met Gly His Phe Leu His Leu  
 50 55 60

Ala Asn Leu Glu Cys Ser Pro Asn Ile Glu Met Phe Leu Cys Gln Ala  
 65 70 75 80

Phe Ile Pro Thr Cys Thr Glu Gln Ile His Val Val Leu Pro Cys Arg  
 85 90 95

Lys Leu Cys Glu Lys Ile Val Ser Asp Cys Lys Lys Leu Met Asp Thr  
 100 105 110

Phe Gly Ile Arg Trp Pro Glu Glu Leu Glu Cys Asn Arg Leu Pro His  
 115 120 125

Cys Asp Asp Thr Val Pro Val Thr Ser His Pro His Thr Glu Leu Ser  
 130 135 140

Gly Pro Gln Lys Lys Ser Asp Gln Val Pro Arg Asp Ile Gly Phe Trp  
 145 150 155 160

Cys Pro Lys His Leu Arg Thr Ser Gly Asp Gln Gly Tyr Arg Phe Leu  
 165 170 175

Gly Ile Glu Gln Cys Ala Pro Pro Cys Pro Asn Met Tyr Phe Lys Ser  
 180 185 190

Asp Glu Leu Asp Phe Ala Lys Ser Phe Ile Gly Ile Val Ser Ile Phe  
 195 200 205

Cys Leu Cys Ala Thr Leu Phe Thr Phe Leu Thr Phe Leu Ile Asp Val  
 210 215 220

Arg Arg Phe Arg Tyr Pro Glu Arg Pro Ile Ile Tyr Tyr Ser Val Cys  
 225 230 235 240  
 Tyr Ser Ile Val Ser Leu Met Tyr Phe Val Gly Phe Leu Leu Gly Asn  
 245 250 255  
 Ser Thr Ala Cys Asn Lys Ala Asp Glu Lys Leu Glu Leu Gly Asp Thr  
 260 265 270  
 Val Val Leu Gly Ser Lys Asn Lys Ala Cys Ser Val Val Phe Met Phe  
 275 280 285  
 Leu Tyr Phe Phe Thr Met Ala Gly Thr Val Trp Trp Val Ile Leu Thr  
 290 295 300  
 Ile Thr Trp Phe Leu Ala Ala Gly Arg Lys Trp Ser Cys Glu Ala Ile  
 305 310 315 320  
 Glu Gln Lys Ala Val Trp Phe His Ala Val Ala Trp Gly Ala Pro Gly  
 325 330 335  
 Phe Leu Thr Val Met Leu Leu Ala Met Asn Lys Val Glu Gly Asp Asn  
 340 345 350  
 Ile Ser Gly Val Cys Phe Val Gly Leu Tyr Asp Leu Asp Ala Ser Arg  
 355 360 365  
 Tyr Phe Val Leu Leu Pro Leu Cys Leu Cys Val Phe Val Gly Leu Ser  
 370 375 380  
 Leu Leu Leu Ala Gly Ile Ile Ser Leu Asn His Val Arg Gln Val Ile  
 385 390 395 400  
 Gln His Asp Gly Arg Asn Gln Glu Lys Leu Lys Lys Phe Met Ile Arg  
 405 410 415  
 Ile Gly Val Phe Ser Gly Leu Tyr Leu Val Pro Leu Val Thr Leu Leu  
 420 425 430  
 Gly Cys Tyr Val Tyr Glu Leu Val Asn Arg Ile Thr Trp Glu Met Thr  
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 Trp Phe Ser Asp His Cys His Gln Tyr Arg Ile Pro Cys Pro Tyr Gln  
 450 455 460

Ala Asn Pro Lys Ala Arg Pro Glu Leu Ala Leu Phe Met Ile Lys Tyr  
 465 470 475 480

Leu Met Thr Leu Ile Val Gly Ile Ser Ala Val Phe Trp Val Gly Ser  
 485 490 495

Lys Lys Thr Cys Thr Glu Trp Ala Gly Phe Phe Lys Arg Asn Arg Lys  
 500 505 510

Arg Asp Pro Ile Ser Glu Ser Arg Arg Val Leu Gln Glu Ser Cys Glu  
 515 520 525

Phe Phe Leu Lys His Asn Ser Lys Val Lys His Lys Lys Lys His Gly  
 530 535 540

Ala Pro Gly Pro His Arg Leu Lys Val Ile Ser Lys Ser Met Gly Thr  
 545 550 555 560

Ser Thr Gly Ala Thr Thr Asn His Gly Thr Ser Ala Met Ala Ile Ala  
 565 570 575

Asp His Asp Tyr Leu Gly Gln Glu Thr Ser Thr Glu Val His Thr Ser  
 580 585 590

Pro Glu Ala Ser Val Lys Glu Gly Arg Ala Asp Arg Ala Asn Thr Pro  
 595 600 605

Ser Ala Lys Asp Arg Asp Cys Gly Glu Ser Ala Gly Pro Ser Ser Lys  
 610 615 620

Leu Ser Gly Asn Arg Asn Gly Arg Glu Ser Arg Ala Gly Gly Leu Lys  
 625 630 635 640

Glu Arg Ser Asn Gly Ser Glu Gly Ala Pro Ser Glu Gly Arg Val Ser  
 645 650 655

Pro Lys Ser Ser Val Pro Glu Thr Gly Leu Ile Asp Cys Ser Thr Ser  
 660 665 670

Gln Ala Ala Ser Ser Pro Glu Pro Thr Ser Leu Lys Gly Ser Thr Ser  
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Ser His Ser Asp Ala  
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<210> 36  
<211> 2039  
<212> DNA  
<213> Homo sapiens

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120

cattatttcc ttaaactcatg ttcgacaagt catacaacat gatggccgga accaagaaaa  
180

actaaagaaa tttatgattc gaattggagt cttcagcggc ttgtatcttg tgccattagt  
240

gacacttctc ggatgttacg tctatgagca agtgaacagg attacctggg agataacttg  
300

ggctctctgat cattgtcgtc agtaccatat cccatgtcct tatcaggcaa aagcaaaagc  
360

tcgaccagaa ttggctttat ttatgataaa atacctgatg acattaattg ttggcatctc  
420

tgctgtcttc tgggttgga gcaaaaagac atgcacagaa tgggctgggt tttttaaacg  
480

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540

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600

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660

cacttctgca gtagcaatta ctagccatga ttacctagga caagaaactt tgacagaaat  
720

ccaaacctca ccagaaacat caatgagaga ggtgaaagcg gacggagcta gcacccccag  
780

gttaagagaa caggactgtg gtgaacctgc ctgccagca gcatccatct ccagactctc  
840

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900

aggaaggatt agtccaaaga gtgatattac tgacactggc ctggcacaga gcaacaattt  
960

gcaggcccc agttcttcag aaccaagcag cctcaaaggt tccacatctc tgcttggtca  
1020



cccggtttca ggagtgagaa aagagcaggg aggtggttgt cattcagata cttgaagaac  
1080

attttctctc gttactcaga agcaaatttg tgttacactg gaagtgacct atgcactgtt  
1140

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1200

ctggaaaaaa tagagttcaa gaataatatg actcatttca cacaaagggt aatgacaaca  
1260

atatacctga aaacagaaaa tgtgcagggt aataatat ttttaatagt gtgggaggac  
1320

agagtttagag gaatcttcct tttctattta tgaagattct actcttggtta agagtatttt  
1380

aagatgtact atgctatttt acttttttga tataaaatca agatatttct ttgctgaagt  
1440

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1500

aacttttttg aaatcctatt caagtatttt tatcatgcta ttgtgatatt ttagcacttt  
1560

ggtagctttt aactgaatt tctaagaaaa ttgtaaaata gtcttctttt atactgtaaa  
1620

aaaagatata ccaaaaagtc ttataatagg aatttaactt taaaaaccca cttattgata  
1680

ccttaccatc taaaatgtgt gatttttata gtctcgtttt aggaatttca cagatctaaa  
1740

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1800

ctcactgatc cttctgcata tttaaaataa aatgtcctaa aggggttagta gacaaaatgt  
1860

tagtcttttg tatattaggc caagtgcaat tgacttcctt tttttaatgt ttcatgacca  
1920

cccattgatt gtattataac cacttacagt tgcttatatt ttttgtttta acttttgttt  
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2039

<210> 37

<211> 706

<212> PRT

<213> Homo sapiens

<400> 37

Met	Glu	Met	Phe	Thr	Phe	Leu	Leu	Thr	Cys	Ile	Phe	Leu	Pro	Leu	Leu
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Met Lys Met Ala Tyr Asn Met Thr Phe Phe Pro Asn Leu Met Gly His  
 35 40 45

Tyr Asp Gln Ser Ile Ala Ala Val Glu Met Glu His Phe Leu Pro Leu  
 50 55 60

Ala Asn Leu Glu Cys Ser Pro Asn Ile Glu Thr Phe Leu Cys Lys Ala  
 65 70 75 80

Phe Val Pro Thr Cys Ile Glu Gln Ile His Val Val Pro Pro Cys Arg  
 85 90 95

Lys Leu Cys Glu Lys Val Tyr Ser Asp Cys Lys Lys Leu Ile Asp Thr  
 100 105 110

Phe Gly Ile Arg Trp Pro Glu Glu Leu Glu Cys Asp Arg Leu Gln Tyr  
 115 120 125

Cys Asp Glu Thr Val Pro Val Thr Phe Asp Pro His Thr Glu Phe Leu  
 130 135 140

Gly Pro Gln Lys Lys Thr Glu Gln Val Gln Arg Asp Ile Gly Phe Trp  
 145 150 155 160

Cys Pro Arg His Leu Lys Thr Ser Gly Gly Gln Gly Tyr Lys Phe Leu  
 165 170 175

Gly Ile Asp Gln Cys Ala Pro Pro Cys Pro Asn Met Tyr Phe Lys Ser  
 180 185 190

Asp Glu Leu Glu Phe Ala Lys Ser Phe Ile Gly Thr Val Ser Ile Phe  
 195 200 205

Cys Leu Cys Ala Thr Leu Phe Thr Phe Leu Thr Phe Leu Ile Asp Val  
 210 215 220

Arg Arg Phe Arg Tyr Pro Glu Arg Pro Ile Ile Tyr Tyr Ser Val Cys  
 225 230 235 240

Tyr Ser Ile Val Ser Leu Met Tyr Phe Ile Gly Phe Leu Leu Gly Asp  
 245 250 255

Ser Thr Ala Cys Asn Lys Ala Asp Glu Lys Leu Glu Leu Gly Asp Thr  
 260 265 270

Val Val Leu Gly Ser Gln Asn Lys Ala Cys Thr Val Leu Phe Met Leu  
 275 280 285

Leu Tyr Phe Phe Thr Met Ala Gly Thr Val Trp Trp Val Ile Leu Thr  
 290 295 300

Ile Thr Trp Phe Leu Ala Ala Gly Arg Lys Trp Ser Cys Glu Ala Ile  
 305 310 315 320

Glu Gln Lys Ala Val Trp Phe His Ala Val Ala Trp Gly Thr Pro Gly  
 325 330 335

Phe Leu Thr Val Met Leu Leu Ala Met Asn Lys Val Glu Gly Asp Asn  
 340 345 350

Ile Ser Gly Val Cys Phe Val Gly Leu Tyr Asp Leu Asp Ala Ser Arg  
 355 360 365

Tyr Phe Val Leu Leu Pro Leu Cys Leu Cys Val Phe Val Gly Leu Ser  
 370 375 380

Leu Leu Leu Ala Gly Ile Ile Ser Leu Asn His Val Arg Gln Val Ile  
 385 390 395 400

Gln His Asp Gly Arg Asn Gln Glu Lys Leu Lys Lys Phe Met Ile Arg  
 405 410 415

Ile Gly Val Phe Ser Gly Leu Tyr Leu Val Pro Leu Val Thr Leu Leu  
 420 425 430

Gly Cys Tyr Val Tyr Glu Gln Val Asn Arg Ile Thr Trp Glu Ile Thr  
 435 440 445

Trp Val Ser Asp His Cys Arg Gln Tyr His Ile Pro Cys Pro Tyr Gln  
 450 455 460

Ala Lys Ala Lys Ala Arg Pro Glu Leu Ala Leu Phe Met Ile Lys Tyr  
 465 470 475 480

Leu Met Thr Leu Ile Val Gly Ile Ser Ala Val Phe Trp Val Gly Ser  
 485 490 495

Lys Lys Thr Cys Thr Glu Trp Ala Gly Phe Phe Lys Arg Asn Arg Lys  
 500 505 510

Arg Asp Pro Ile Ser Glu Ser Arg Arg Val Leu Gln Glu Ser Cys Glu  
 515 520 525

Phe Phe Leu Lys His Asn Ser Lys Val Lys His Lys Lys Lys His Tyr  
 530 535 540

Lys Pro Ser Ser His Lys Leu Lys Val Ile Ser Lys Ser Met Gly Thr  
 545 550 555 560

Ser Thr Gly Ala Thr Ala Asn His Gly Thr Ser Ala Val Ala Ile Thr  
 565 570 575

Ser His Asp Tyr Leu Gly Gln Glu Thr Leu Thr Glu Ile Gln Thr Ser  
 580 585 590

Pro Glu Thr Ser Met Arg Glu Val Lys Ala Asp Gly Ala Ser Thr Pro  
 595 600 605

Arg Leu Arg Glu Gln Asp Cys Gly Glu Pro Ala Ser Pro Ala Ala Ser  
 610 615 620

Ile Ser Arg Leu Ser Gly Glu Gln Val Asp Gly Lys Gly Gln Ala Gly  
 625 630 635 640

Ser Val Ser Glu Ser Ala Arg Ser Glu Gly Arg Ile Ser Pro Lys Ser  
 645 650 655

Asp Ile Thr Asp Thr Gly Leu Ala Gln Ser Asn Asn Leu Gln Val Pro  
 660 665 670

Ser Ser Ser Glu Pro Ser Ser Leu Lys Gly Ser Thr Ser Leu Leu Val  
 675 680 685

His Pro Val Ser Gly Val Arg Lys Glu Gln Gly Gly Gly Cys His Ser  
 690 695 700

Asp Thr  
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<210> 38  
 <211> 773  
 <212> DNA  
 <213> Murinae gen. sp.

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180  
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240  
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420  
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480  
gaactacatc agaacggtaa gcacgacgat ctcccgcgtg cttctcatcc cctgattgct  
540  
ggagacagag aaggacgctc accagatcaa tagagacgca tcataacgca acgccgcgaa  
600  
ggctttctgct cctcttcaag ctgtagatgc tgtcaatctt gctgccctcg gggctctgtg  
660  
gcatccgtta actttgcttt tccgggaaga aaaatgtctt gtgctaagct ccaccctcg  
720  
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773

<210> 39  
<211> 852  
<212> DNA  
<213> Murinae gen. sp.

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120  
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180  
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240  
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300

tgccgccttc gccggactga tgtacctgtt tgtgaggcaa aaatactttg tcggctatct  
360

gggagagaga actcagagca cccctggcta catcttcggc aagcggatca tcctgttcct  
420

gttcctcatg tccttcgccg ggataactcaa ccattacctc atcttcttct tcggaagcga  
480

ctttgagaac tacatcagaa cggtaagcac gacgatctcc ccgctgcttc tcatcccctg  
540

attgctggag acagagaagg acgctcacca gatcaataga gacgcatcat aacgcaacgc  
600

cgogaaggct tctgctcctc ttcaagctgt agatgctgtc aatcttgctg ccctcggggc  
660

tctgtggcat ccgttaactt tgcttttccg ggaagaaaaa tgtcttgtgc tagctccacc  
720

cctogaatgc ggcggtggcc caggatttat tgtctacatc cagcctatac ttctcctggc  
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852

<210> 40  
<211> 161  
<212> PRT  
<213> Murinae gen. sp.

<400> 40

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Leu	Ile	Ser	Val	Val	Gln	Asn	Val	Phe	Phe	Ala	His	Tyr	Val	Glu	His
			20					25					30		

Glu	Ser	Asn	Ala	His	Asn	Gly	Arg	Ser	Phe	Gln	Arg	Thr	Gly	Thr	Leu
		35					40					45			

Ala	Phe	Glu	Arg	Val	Tyr	Thr	Ala	Asn	Gln	Asn	Cys	Val	Asp	Ala	Tyr
	50					55					60				

Pro	Thr	Phe	Leu	Val	Val	Leu	Trp	Thr	Ala	Gly	Leu	Leu	Cys	Ser	Gln
65					70					75					80

Val	Pro	Ala	Ala	Phe	Ala	Gly	Leu	Met	Tyr	Leu	Phe	Val	Arg	Gln	Lys
				85					90					95	

Tyr Phe Val Gly Tyr Leu Gly Glu Arg Thr Gln Ser Thr Pro Gly Tyr  
 100 105 110

Ile Phe Gly Lys Arg Ile Ile Leu Phe Leu Phe Leu Met Ser Phe Ala  
 115 120 125

Gly Ile Leu Asn His Tyr Leu Ile Phe Phe Phe Gly Ser Asp Phe Glu  
 130 135 140

Asn Tyr Ile Arg Thr Val Ser Thr Thr Ile Ser Pro Leu Leu Leu Ile  
 145 150 155 160

Pro

<210> 41  
 <211> 873  
 <212> DNA  
 <213> Homo sapiens

<400> 41  
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agcctgaagc aaacatggat caagaaactg taggcaatgt tgtcctgttg gccatcgta  
 120

ccctcatcag cgtgggtccag aatggattct ttgccataa agtggagcac gaaagcagga  
 180

cccagaatgg gaggagcttc cagaggaccg gaacacttgc ctttgagcgg gtctacactg  
 240

ccaaccagaa ctgtgtagat gcgtacccca ctttcctcgc tgtgctctgg tctgcggggc  
 300

tactttgcag ccaagttcct gctgcgtttg ctggactgat gtacttgttt gtgaggcaaa  
 360

agtactttgt cggttacctt ggagagagaa cgcagagcac ccctggctac atatttgga  
 420

aacgcatcat actcttcctg ttctcatgt ccgttgctgg catattcaac tattacctca  
 480

tcttcttttt cggaagtgc tttgaaaact acataaagac gatctccacc accatctccc  
 540

ctctacttct cattccctaa ctctctgctg aatatggggg tgggtgttct atctaataa  
 600

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 660

aaatctattg gccatctggg cttcacagct tgagttaacc ttgcttttcc gggaacaaaa  
720

tgatgtcatg tcagctccgc cccttgaaca tgaccgtggc cccaaatttg ctattcccat  
780

gcattttgtt tgtttcttca cttatcctgt tctctgaaga tgttttgtga ccaggtttgt  
840

gttttcttaa aataaaatgc agagacatgt ttt  
873

<210> 42  
<211> 161  
<212> PRT  
<213> Homo sapiens

<400> 42

Met Asp Gln Glu Thr Val Gly Asn Val Val Leu Leu Ala Ile Val Thr  
1 5 10 15

Leu Ile Ser Val Val Gln Asn Gly Phe Phe Ala His Lys Val Glu His  
20 25 30

Glu Ser Arg Thr Gln Asn Gly Arg Ser Phe Gln Arg Thr Gly Thr Leu  
35 40 45

Ala Phe Glu Arg Val Tyr Thr Ala Asn Gln Asn Cys Val Asp Ala Tyr  
50 55 60

Pro Thr Phe Leu Ala Val Leu Trp Ser Ala Gly Leu Leu Cys Ser Gln  
65 70 75 80

Val Pro Ala Ala Phe Ala Gly Leu Met Tyr Leu Phe Val Arg Gln Lys  
85 90 95

Tyr Phe Val Gly Tyr Leu Gly Glu Arg Thr Gln Ser Thr Pro Gly Tyr  
100 105 110

Ile Phe Gly Lys Arg Ile Ile Leu Phe Leu Phe Leu Met Ser Val Ala  
115 120 125

Gly Ile Phe Asn Tyr Tyr Leu Ile Phe Phe Phe Gly Ser Asp Phe Glu  
130 135 140

Asn Tyr Ile Lys Thr Ile Ser Thr Thr Ile Ser Pro Leu Leu Leu Ile  
145 150 155 160

Pro



<210> 43  
<211> 803  
<212> DNA  
<213> Murinae gen. sp.

<400> 43  
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120  
tacggaacac atttcatggt tcctttgaag agttaagaga agaaagtatt tgtaagaaca  
180  
ggaaaagaaa caaatacttt gcaaataaac tggctgctgc tgtgaccaca tctgaatagc  
240  
aaaggcgatc gatcaagcgc tgcggacaaa aggcctcctg taagctgcac tgctgacaa  
300  
tggtaagctc caatggctcc cagtgccctt atgacgactc ctttaagtac actctgtacg  
360  
ggatgcatgtt cagcatgggtc ttcgtgcttg ggctgatatc caactgtgtt gcgatataca  
420  
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480  
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540  
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660  
ccatttaagt caaagacttt aagaaacgaa acgaaaatgc aaagaatcgt ttgcattgcc  
720  
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780  
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803

<210> 44  
<211> 1849  
<212> DNA  
<213> Murinae gen. sp.

<400> 44  
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120

atcaatgtag aaatacaaag tttgagaata aaaagaagga agaagtaccc gaggacgacg  
180

ggcggacgga cgcacggcga gtgtttgtga ctgaagtaaa gctggtttgg accctggcgg  
240

ctgaagcaca agtttccacg cggactggtc tgggtccgact tggaacagtt tttccttaca  
300

ctttcagctt tatgggttgg cttccttgac tgcattttct gtcagttaac taaactccag  
360

actcatggat tttctcgacc agaaaatcag actattttcc tgaataatct actagaaact  
420

tttacggaac acatttcatg tttcctttga agagttaaga gaagaaagta tttgtaagaa  
480

caggaaaaga aacaaataact ttgcaaataa actggctgct gctgtgacca catctgaata  
540

gcaaaggcga tcgatcaagc gctgcggaca aaaggcctcc tgtaagctgc actgcctgac  
600

aatggtaagc tccaatggct cccagtgcc ttatgacgac tcctttaagt aactctgtga  
660

cgggtgcatg ttcagcatgg tcttcgtgct tgggctgata tccaactgtg ttgcgatata  
720

cattttcatc tgtgccctca aagtgagaaa tgaaactaca acgtacatga ttaacctggc  
780

aatgtcagat ttacttttctg tctttacttt gccatttcgg attttttact ttgcaacacg  
840

gaattggcca tttggagatc tactctgtaa gatttcagta atgctgtttt acaccaatat  
900

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960

cccattttaag tcaaagactt taagaacgaa acgaaatgca aagatcgttt gcattgctgt  
1020

gtggttcaca gtgatgggag gaagtgcgcc tgcagttttc tttcagtcga cccactctca  
1080

ggggaacaat acctcagaag cctgctttga gaactttcca gcggccacat ggaaaactta  
1140

tctctccagg attgtgattt tcattgaaat agtgggcttt tttatccctc tcattttgaa  
1200

cgtaacttgt tctagtatgg tgctaagaac tttaaataaa cctgttacat taagtagaag  
1260

caaaatgaac aaaactaagg ttttaaaaat gatttttgtc cacttgggtca tcttctgttt  
1320

ctgtttttgtg ccctacaaca tcaacctcat tttgtactcg ctcatgagga cacagacctt  
1380

tgtttaactgc tctgtgggtgg cggcagtgag gaccatgtac ccgatcactc tctgcatcgc  
1440

tgtttccaac tgctgctttg accctattgt ttactacttc acctcagaca caattcagaa  
1500

ctcaataaaaa atgaaaaact ggtcgggttag aagaagtgc tccagggttct ctgaagttca  
1560

gggcactgag aatttttatcc aacacaacct acagacctta aaaaataaga tatttgataa  
1620

tgaatctgca atataagctg cctgactaag ccactgggac tgctccgtgt tcaactgtga  
1680

aaactgtgtt cttgggaact atctctccgg ctccaacaga aaatattttt aaaggaagtt  
1740

tgtgtctgat gtgttaaaca ttaaaatata ttctattctt gtatgcacgc cattttactt  
1800

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1849

<210> 45

<211> 316

<212> PRT

<213> Murinae gen. sp.

<400> 45

Asp	Asp	Ser	Phe	Lys	Tyr	Thr	Leu	Tyr	Gly	Cys	Met	Phe	Ser	Met	Val
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Phe	Val	Leu	Gly	Leu	Ile	Ser	Asn	Cys	Val	Ala	Ile	Tyr	Ile	Phe	Ile
		20						25					30		

Cys	Ala	Leu	Lys	Val	Arg	Asn	Glu	Thr	Thr	Thr	Tyr	Met	Ile	Asn	Leu
		35					40					45			

Ala	Met	Ser	Asp	Leu	Leu	Phe	Val	Phe	Thr	Leu	Pro	Phe	Arg	Ile	Phe
	50					55					60				

Tyr	Phe	Ala	Thr	Arg	Asn	Trp	Pro	Phe	Gly	Asp	Leu	Leu	Cys	Lys	Ile
65					70					75					80

Ser	Val	Met	Leu	Phe	Tyr	Thr	Asn	Met	Tyr	Gly	Ser	Ile	Leu	Phe	Leu
				85					90						95

Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe Lys  
 100 105 110

Ser Lys Thr Leu Arg Thr Lys Arg Asn Ala Lys Ile Val Cys Ile Ala  
 115 120 125

Val Trp Phe Thr Val Met Gly Gly Ser Ala Pro Ala Val Phe Phe Gln  
 130 135 140

Ser Thr His Ser Gln Gly Asn Asn Thr Ser Glu Ala Cys Phe Glu Asn  
 145 150 155 160

Phe Pro Ala Ala Thr Trp Lys Thr Tyr Leu Ser Arg Ile Val Ile Phe  
 165 170 175

Ile Glu Ile Val Gly Phe Phe Ile Pro Leu Ile Leu Asn Val Thr Cys  
 180 185 190

Ser Ser Met Val Leu Arg Thr Leu Asn Lys Pro Val Thr Leu Ser Arg  
 195 200 205

Ser Lys Met Asn Lys Thr Lys Val Leu Lys Met Ile Phe Val His Leu  
 210 215 220

Val Ile Phe Cys Phe Cys Phe Val Pro Tyr Asn Ile Asn Leu Ile Leu  
 225 230 235 240

Tyr Ser Leu Met Arg Thr Gln Thr Phe Val Asn Cys Ser Val Val Ala  
 245 250 255

Ala Val Arg Thr Met Tyr Pro Ile Thr Leu Cys Ile Ala Val Ser Asn  
 260 265 270

Cys Cys Phe Asp Pro Ile Val Tyr Tyr Phe Thr Ser Asp Thr Ile Gln  
 275 280 285

Asn Ser Ile Lys Met Lys Asn Trp Ser Val Arg Arg Ser Asp Ser Arg  
 290 295 300

Phe Ser Glu Val Gln Gly Thr Glu Asn Phe Ile Gln  
 305 310 315

<210> 46  
 <211> 1035  
 <212> DNA  
 <213> Homo sapiens

<400> 46  
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120  
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180  
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240  
aattggccat ttggagattt actttgtaag atttctgtga tgctgtttta taccaacatg  
300  
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360  
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420  
tggttaactg tgatcggagg aagtgcaccc gccgtttttg ttcagtctac ccactctcag  
480  
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540  
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gtaacttggt ctagtatggg gctaaaaact ttaaccaaac ctgttacatt aagtagaagc  
660  
aaaataaaca aaactaagggt tttaaaaatg atttttgtac atttgatcat attctgtttc  
720  
tgttttgttc cttacaatat caatcttatt ttatattctc ttgtgagaac acaaacattt  
780  
gttaattgct cagtagtggc agcagtaagg acaatgtacc caatcactct ctgtattgct  
840  
gtttccaact gttgttttga ccctatagtt tactacttta catcggacac aattcagaat  
900  
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960  
ggcgcagaga attttattca gcataaccta cagaccttaa aaagtaagat atttgacaat  
1020  
gaatctgctg cctga  
1035

<210> 47  
<211> 344  
<212> PRT  
<213> Homo sapiens

&lt;400&gt; 47

Met Val Ser Val Asn Ser Ser His Cys Phe Tyr Asn Asp Ser Phe Lys  
 1 5 10 15

Tyr Thr Leu Tyr Gly Cys Met Phe Ser Met Val Phe Val Leu Gly Leu  
 20 25 30

Ile Ser Asn Cys Val Ala Ile Tyr Ile Phe Ile Cys Val Leu Lys Val  
 35 40 45

Arg Asn Glu Thr Thr Thr Tyr Met Ile Asn Leu Ala Met Ser Asp Leu  
 50 55 60

Leu Phe Val Phe Thr Leu Pro Phe Arg Ile Phe Tyr Phe Thr Thr Arg  
 65 70 75 80

Asn Trp Pro Phe Gly Asp Leu Leu Cys Lys Ile Ser Val Met Leu Phe  
 85 90 95

Tyr Thr Asn Met Tyr Gly Ser Ile Leu Phe Leu Thr Cys Ile Ser Val  
 100 105 110

Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe Lys Ser Lys Thr Leu Arg  
 115 120 125

Thr Lys Arg Asn Ala Lys Ile Val Cys Thr Gly Val Trp Leu Thr Val  
 130 135 140

Ile Gly Gly Ser Ala Pro Ala Val Phe Val Gln Ser Thr His Ser Gln  
 145 150 155 160

Gly Asn Asn Ala Ser Glu Ala Cys Phe Glu Asn Phe Pro Glu Ala Thr  
 165 170 175

Trp Lys Thr Tyr Leu Ser Arg Ile Val Ile Phe Ile Glu Ile Val Gly  
 180 185 190

Phe Phe Ile Pro Leu Ile Leu Asn Val Thr Cys Ser Ser Met Val Leu  
 195 200 205

Lys Thr Leu Thr Lys Pro Val Thr Leu Ser Arg Ser Lys Ile Asn Lys  
 210 215 220

Thr Lys Val Leu Lys Met Ile Phe Val His Leu Ile Ile Phe Cys Phe  
 225 230 235 240

Cys Phe Val Pro Tyr Asn Ile Asn Leu Ile Leu Tyr Ser Leu Val Arg  
 245 250 255

Thr Gln Thr Phe Val Asn Cys Ser Val Val Ala Ala Val Arg Thr Met  
 260 265 270

Tyr Pro Ile Thr Leu Cys Ile Ala Val Ser Asn Cys Cys Phe Asp Pro  
 275 280 285

Ile Val Tyr Tyr Phe Thr Ser Asp Thr Ile Gln Asn Ser Ile Lys Met  
 290 295 300

Lys Asn Trp Ser Val Arg Arg Ser Asp Phe Arg Phe Ser Glu Val His  
 305 310 315 320

Gly Ala Glu Asn Phe Ile Gln His Asn Leu Gln Thr Leu Lys Ser Lys  
 325 330 335

Ile Phe Asp Asn Glu Ser Ala Ala  
 340

<210> 48  
 <211> 814  
 <212> DNA  
 <213> Murinae gen. sp.

<400> 48  
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ggccaggcct agcacatgta cctcacagac caactggcaa gcagccttca gggagctcga  
 120

tccccaaaca gccagtcacc acctctgtcc cctcttcaact gttggtcgtc agactgcctg  
 180

agtggacagc aggctggctg cgttgtatct tcaacttcctt cctctgactg gcttgctctt  
 240

gtctctcagt ctttcatccc aggcagctgc ctgaggtagg tgaggaggat ggtgagccag  
 300

gcaggtctac aataaaggca gctctgtccg gctccttctg gctcgtgagt gtcaccggcc  
 360

tggaagactg agggaatggc tccccctctt cctccccgtc tttccccagt tccttcctta  
 420

tggtggccca tgtgccagg gagttggaag catcaggag accctcttag tgtggggaag  
 480

gaagtcagag accattgaca cagtgaagag gcaggatcat gtgttggaag cctgttagca  
540

ggaccaaggt gactcttggg agagactctt gtggacacag gccgtggtgg cttgtcagac  
600

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660

gggacactgc tgagtaatga gcagcttatt acacacaatg ggaagagggg cagagagggc  
720

tgtgtcggtt gagtctcggc tgggactgaa gtttgccata agtagtggtt gtacatccag  
780

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<210> 49

<211> 1164

<212> DNA

<213> Murinae gen. sp.

<400> 49

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120

cagcccagcc tcttgggggt caggagggtc ctgcagaaac tccagacgga cggactcaag  
180

gagtgcatta tcttctgcgt gcgggaggag cctgtggtgt tcttgcgcgc tgaggaggac  
240

tttgtgtctt acacacctcg agacaaggag agccttcatg agaacctcag ggaccctagt  
300

ccaggggtca aggctgagaa tctggagctg gccatccaga aagagatcca tgactttgcc  
360

caattgagag ataatgtgta ccacgtatac cacaacacag aggacctgcg cggggagccg  
420

cacaccgtgg ccatccgagg tgaggatggc gtgtgcgtga ccgaggaggt gtttaagcgg  
480

ccgctcttcc tgcagccac ctacagatac caccgctcc ccttgccaga gcaaggggcc  
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cccctggaag ccagtttga tgcctttgtc agcgttcttc gggagacccc cagccttctg  
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ggcagaacca acctaggcat gtcctggga accctcgtca tgttccacca cagtaggacc  
720



acctcccagc tagaggcagc ctccccgttg gccaaacccc tgcccatgga gcagtttcag  
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960

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1020

tatctgcatg agcagtaccc cctggccttt gccctcagtt tcagtcgatg gctgtgtacc  
1080

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1164

<210> 50  
<211> 388  
<212> PRT  
<213> Murinae gen. sp.

<400> 50

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Gly	Thr	Leu	Lys	Ser	Cys	Gly	Ala	Pro	Asn	Phe	Arg	Gln	Val	Arg	Gly
			20					25					30		

Gly	Leu	Pro	Val	Phe	Gly	Met	Gly	Gln	Pro	Ser	Leu	Leu	Gly	Phe	Arg
		35					40						45		

Arg	Val	Leu	Gln	Lys	Leu	Gln	Thr	Asp	Gly	Leu	Lys	Glu	Cys	Ile	Ile
	50					55					60				

Phe	Cys	Val	Arg	Glu	Glu	Pro	Val	Val	Phe	Leu	Arg	Ala	Glu	Glu	Asp
65					70					75					80

Phe	Val	Ser	Tyr	Thr	Pro	Arg	Asp	Lys	Glu	Ser	Leu	His	Glu	Asn	Leu
				85					90					95	

Arg	Asp	Pro	Ser	Pro	Gly	Val	Lys	Ala	Glu	Asn	Leu	Glu	Leu	Ala	Ile
			100					105						110	

Gln	Lys	Glu	Ile	His	Asp	Phe	Ala	Gln	Leu	Arg	Asp	Asn	Val	Tyr	His
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115	120	125
Val Tyr His Asn Thr Glu Asp Leu Arg Gly Glu Pro His Thr Val Ala		
130	135	140
Ile Arg Gly Glu Asp Gly Val Cys Val Thr Glu Glu Val Phe Lys Arg		
145	150	155
Pro Leu Phe Leu Gln Pro Thr Tyr Arg Tyr His Arg Leu Pro Leu Pro		
	165	170
		175
Glu Gln Gly Ala Pro Leu Glu Ala Gln Phe Asp Ala Phe Val Ser Val		
	180	185
		190
Leu Arg Glu Thr Pro Ser Leu Leu Pro Leu Arg Asp Asn His Gly Pro		
	195	200
		205
Leu Pro Ala Leu Leu Phe Ser Cys Gln Ser Gly Val Gly Arg Thr Asn		
	210	215
		220
Leu Gly Met Val Leu Gly Thr Leu Val Met Phe His His Ser Arg Thr		
225	230	235
		240
Thr Ser Gln Leu Glu Ala Ala Ser Pro Leu Ala Lys Pro Leu Pro Met		
	245	250
		255
Glu Gln Phe Gln Val Ile Gln Gly Phe Ile Cys Lys Val Pro Gln Gly		
	260	265
		270
Lys Lys Met Val Glu Glu Val Asp Arg Ala Ile Ser Ala Cys Ala Glu		
	275	280
		285
Leu His Asp Leu Lys Glu Glu Val Leu Lys Asn Gln Arg Arg Leu Glu		
	290	295
		300
Ser Phe Arg Pro Glu Ser Arg Gly Gln Glu Cys Gly Ser Gln Gln Ala		
305	310	315
		320
Val Gln Gln Arg Ala Leu Trp Ser Leu Glu Leu Tyr Phe Tyr Leu Leu		
	325	330
		335
Leu Phe Asn Tyr Tyr Leu His Glu Gln Tyr Pro Leu Ala Phe Ala Leu		
	340	345
		350
Ser Phe Ser Arg Trp Leu Cys Thr His Pro Glu Leu Tyr Arg Leu Leu		
	355	360
		365

Val Glu Leu Asn Ser Val Gly Pro Leu Val Pro Gly Asp Leu Ile Ala  
 370 375 380

Lys Gly Ser Leu  
 385

<210> 51  
 <211> 4303  
 <212> DNA  
 <213> Homo sapiens

<400> 51  
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 accccatttg agggcctaca gggcagtggc acgatggaca gtcggcactc cgtcagcatc  
 120  
 cactccttcc agagcactag cttgcataac agcaaggcca agtccatcat cccaacaag  
 180  
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 240  
 ctcaaggctc attacacgtt gggccggctc tcggacaaca ccctgagca ctacctggtg  
 300  
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 420  
 ggacagccca gcctctcagg gttcaggcgg gtcctccaga aactccagaa ggacggacat  
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 720  
 ccccatgctg tggccatcca tggtagaggac gacttgcatt tgacggagga ggtgtacaag  
 780  
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 900

ctgcagctcc gtgatgccca cgggcctccc ccagccctcg tcttcagctg ccagatgggc  
960

gtgggcagga ccaacctggg catggtcctg ggcacctca tcctgcttca ccgcagtggg  
1020

accacctccc agccagaggc tgccccacg caggccaagc ccctgcctat ggagcagttc  
1080

caggtgatcc agagctttct ccgcatgggtg ccccagggaa ggaggatggg ggaagagggt  
1140

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1200

cagaagaagt tagaaggat cgcaccggag agcccagccc agggaagcgg cagccgacac  
1260

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Asp Ser Arg His Ser Val Ser Ile His Ser Phe Gln Ser Thr Ser Leu  
 35 40 45

His Asn Ser Lys Ala Lys Ser Ile Ile Pro Asn Lys Val Ala Pro Val  
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Val Ile Thr Tyr Asn Cys Lys Glu Glu Phe Gln Ile His Asp Glu Leu  
 65 70 75 80

Leu Lys Ala His Tyr Thr Leu Gly Arg Leu Ser Asp Asn Thr Pro Glu  
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His Tyr Leu Val Gln Gly Arg Tyr Phe Leu Val Arg Asp Val Thr Glu  
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Lys Met Asp Val Leu Gly Thr Val Gly Ser Cys Gly Ala Pro Asn Phe  
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Arg Gln Val Gln Gly Gly Leu Thr Val Phe Gly Met Gly Gln Pro Ser  
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Leu Ser Gly Phe Arg Arg Val Leu Gln Lys Leu Gln Lys Asp Gly His  
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Arg Ala Asp Glu Asp Phe Val Ser Tyr Thr Pro Arg Asp Lys Gln Asn  
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Leu His Glu Asn Leu Gln Gly Leu Gly Pro Gly Val Arg Val Glu Ser  
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Leu Glu Leu Ala Ile Arg Lys Glu Ile His Asp Phe Ala Gln Leu Ser  
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Glu Asn Thr Tyr His Val Tyr His Asn Thr Glu Asp Leu Trp Gly Glu  
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Pro His Ala Val Ala Ile His Gly Glu Asp Asp Leu His Val Thr Glu  
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Glu Val Tyr Lys Arg Pro Leu Phe Leu Gln Pro Thr Tyr Arg Tyr His  
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Val Gly Arg Thr Asn Leu Gly Met Val Leu Gly Thr Leu Ile Leu Leu  
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Met Val Pro Gln Gly Arg Arg Met Val Glu Glu Val Asp Arg Ala Ile  
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Leu Ala Phe Ala Leu Ser Phe Ser Arg Trp Leu Cys Ala His Pro Glu  
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Leu Tyr Arg Leu Pro Val Thr Leu Ser Ser Ala Gly Pro Val Ala Pro  
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Arg Asp Leu Ile Ala Arg Gly Ser Leu Arg Glu Asp Asp Leu Val Ser  
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Pro Asp Ala Leu Ser Thr Val Arg Glu Met Asp Val Ala Asn Phe Arg  
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Pro Pro Pro Gly Lys Glu Gly Pro Leu Thr Tyr Arg Phe Gln Thr Cys  
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Leu Thr Tyr His Arg Ile Pro Met Pro Asp Phe Cys Ala Pro Arg Glu  
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Glu Asp Phe Asp Gln Leu Leu Glu Ala Leu Arg Ala Ala Leu Ser Lys  
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Thr Thr Thr Ala Met Val Val Ala Val Leu Ala Phe Trp His Ile Gln  
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Gly Phe Pro Glu Val Gly Glu Glu Glu Leu Val Ser Val Pro Asp Ala  
 690 695 700

Lys Phe Thr Lys Gly Glu Phe Gln Val Val Met Lys Val Val Gln Leu  
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Leu Pro Asp Gly His Arg Val Lys Lys Glu Val Asp Ala Ala Leu Asp  
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Thr Val Ser Glu Thr Met Thr Pro Met His Tyr His Leu Arg Glu Ile

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Ser	Cys	Ser	Leu	Glu	Pro	Ser	Ala	Pro	Glu	Asp	Leu	Leu					
	850					855					860						